

Amendments to the Specification:

Please replace the word "Disucussion" between paragraphs [0191] and [0192] of the published application U.S.20070054849 with "Discussion".

Please replace paragraph [0114] with the following amended paragraph:

-- [A'] is a ribonucleotide sequence consisting of the complementary sequence of [A]. The region [A] hybridizes to [A'], and then a loop consisting of region [B] is formed. The loop sequence may be preferably 3 to 23 nucleotide in length. The loop sequence, for example, can be selected from group consisting of following sequences (<http://www.ambion.com/techlib/tb/tb.sub.--506.html>). Furthermore, loop sequence consisting of 23 nucleotides also provides active siRNA (Jacque, J.-M., Triques, K., and Stevenson, M. (2002) Modulation of HIV-1 replication by RNA interference. Nature 418: 435-438.).--

Please replace paragraph [0123] with the following amended paragraph:

-- The nucleotide sequence of suitable siRNAs can be designed using a siRNA design computer program available from the Ambion website (http://www.ambion.com/techlib/misc/siRNA_finder.html). The computer program selects nucleotide sequences for siRNA synthesis based on the following protocol.--

Please replace paragraph [0184] with the following amended paragraph:

-- The expression profiles of 20 HCCs were compared with their corresponding non-cancerous liver tissues using cDNA microarray containing 23,040 genes. Among commonly up-regulated genes in HCCs, a gene with an in-house accession number of D4999, corresponding to an EST (MGC47816) in Hs.420244 of a UniGene cluster (<http://www.ncbi.nlm.nih.gov/UniGene/>), was over-expressed in seven of eleven HCCs compared with the corresponding noncancerous liver tissues (FIG. 1). To clarify the results of the microarray, semi-quantitative RT-PCR we performed, which revealed that expression of

D4999 was increased in seven of additional eight HCCs as compared with corresponding non-cancerous liver tissues (FIG. 2).--

Please replace paragraph [0185] with the following amended paragraph:

-- Homology searches with the sequence of D4999 in public databases using BLAST program in National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/BLAST/>) identified ESTs including MGC47816 (GenBank accession number of NM.sub.--173642) and a genomic sequence with GenBank accession number of AA971400 assigned to chromosomal band 1q34.1. Comparison of MGC47816 cDNA and the genomic sequence disclosed that this gene consisted of 5 exons. The putative full-length cDNA consisted of 1528 nucleotides, with an open reading frame of 1176 nucleotides (SEQ ID NO: 1) encoding a 391-amino-acid protein (SEQ ID NO: 2). The amino acid sequence of the predicted MGC47816 protein showed 88% identity to a mouse hypothetical protein B930030J24. A search for protein motifs with the Simple Modular Architecture Research Tool (SMART, <http://smart.embl-heidelberg.de>) revealed that the predicted protein contained a carbamoyl-phosphate synthase L chain and an ATP binding domain (codons 71-253) (FIG. 3).--

Please replace paragraph [0188] with the following amended paragraph:

-- The expression profiles of 20 HCCs were analyzed with the corresponding non-cancerous liver tissues using the cDNA microarray containing 23,040 genes. Among commonly up-regulated genes in HCCs, a gene with an in-house accession number of C2298, corresponding to HES6 (Hs.42949 of a UniGene cluster at <http://www.ncbi.nlm.nih.gov/UniGene/>), was over-expressed in eleven of twelve HCCs compared with the corresponding noncancerous liver tissues (FIG. 6a). To clarify the results of the microarray, semi-quantitative RT-PCR was performed, which revealed that expression of HES6 was increased in 7 out of additional 8 HCCs as compared with corresponding non-cancerous liver tissues (FIG. 6b).--

Please replace paragraph [0189] with the following amended paragraph:

-- Homology searches with the sequence of C2298 in public databases using BLAST program in National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/BLAST/>) identified cDNA sequences including GenBank accession number BC007939 that corresponded to HES6, and a genomic sequence with GenBank accession number of AA357675 assigned to chromosomal band 2q37. The HES6 cDNA sequence consisted of 1375 nucleotides containing an open reading frame of 675 nucleotides (SEQ ID NO: 27) encoding a putative 224-amino-acid protein (SEQ ID NO: 28) (GenBank accession number BC007939). The first ATG was flanked by a sequence (GGCATGG) that agreed with the consensus sequence for initiation of translation in eukaryotes. Comparison of HES6 cDNA and the genomic sequence disclosed that this gene consisted of 4 exons. Additionally, multiple-Tissue Northern-blot analysis was performed using a PCR product of HES6 as a probe, and detected a 1.4 kb-transcript that was expressed in testis, spinal cord and skeletal muscle (FIG. 7). A search for protein motifs with the Simple Modular Architecture Research Tool (SMART, <http://smart.emblheidelberg.de>) revealed that the predicted protein contained a helix-loop-helix domain and orange domain (codons 31-80, 94-135) (FIG. 8).--